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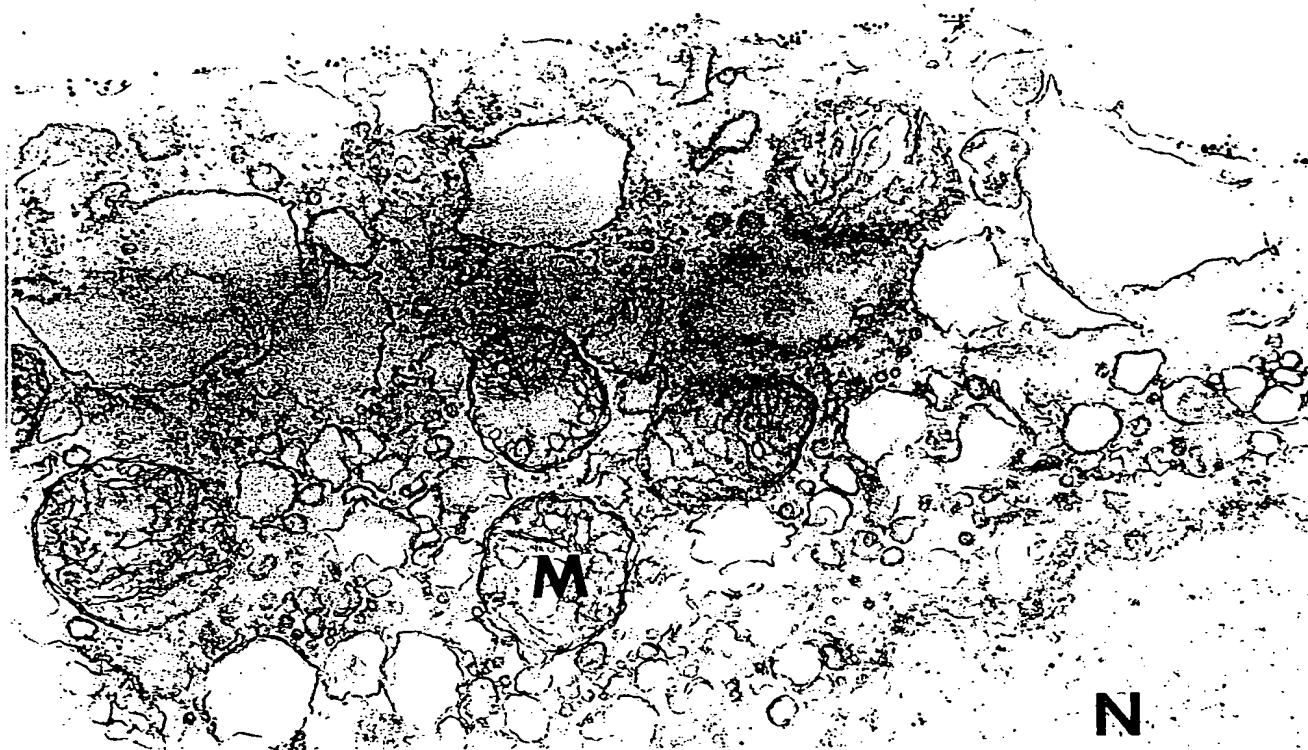


FIGURE 1

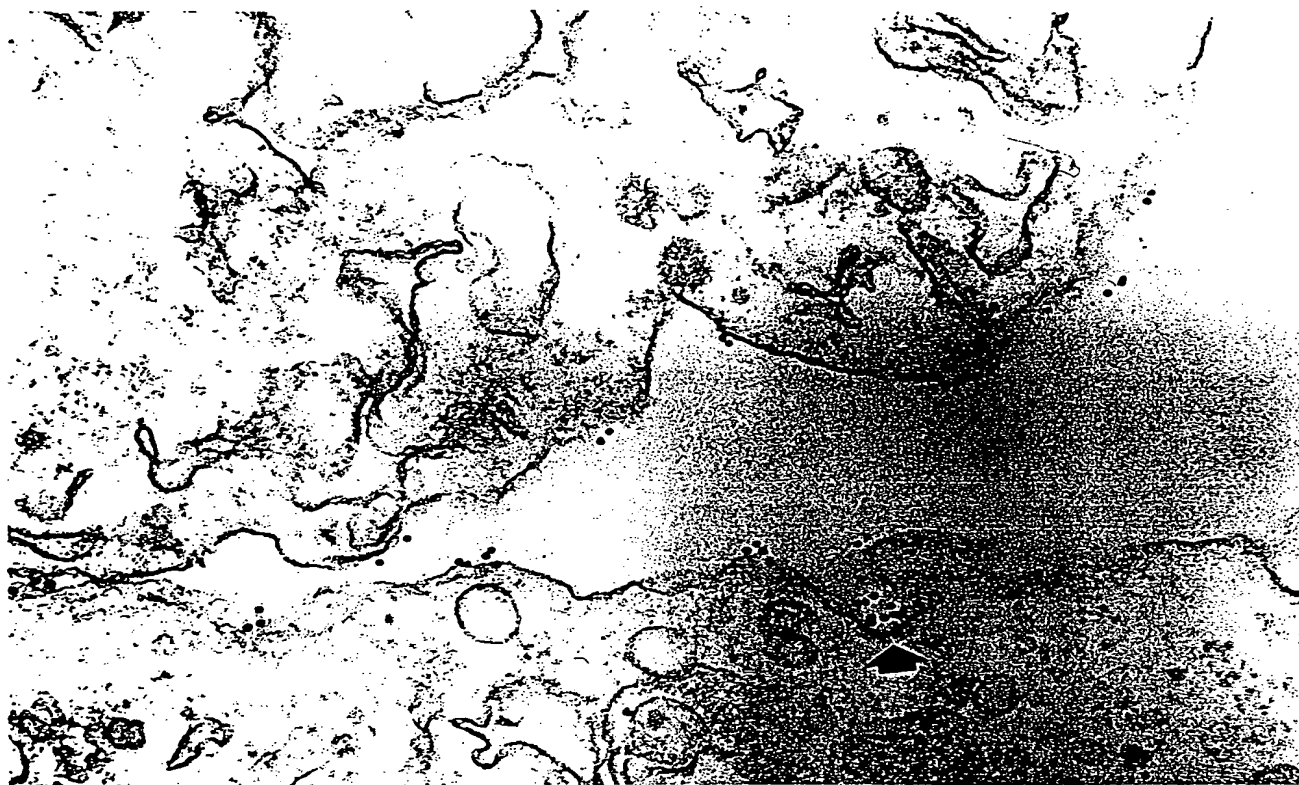


FIGURE 2

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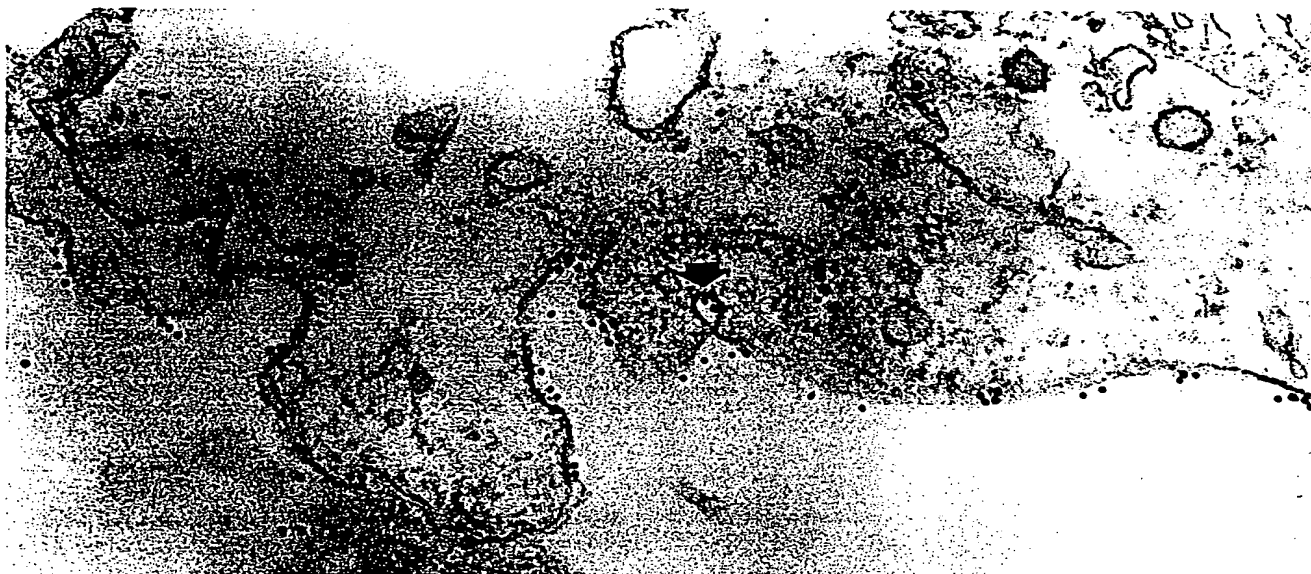


FIGURE 3

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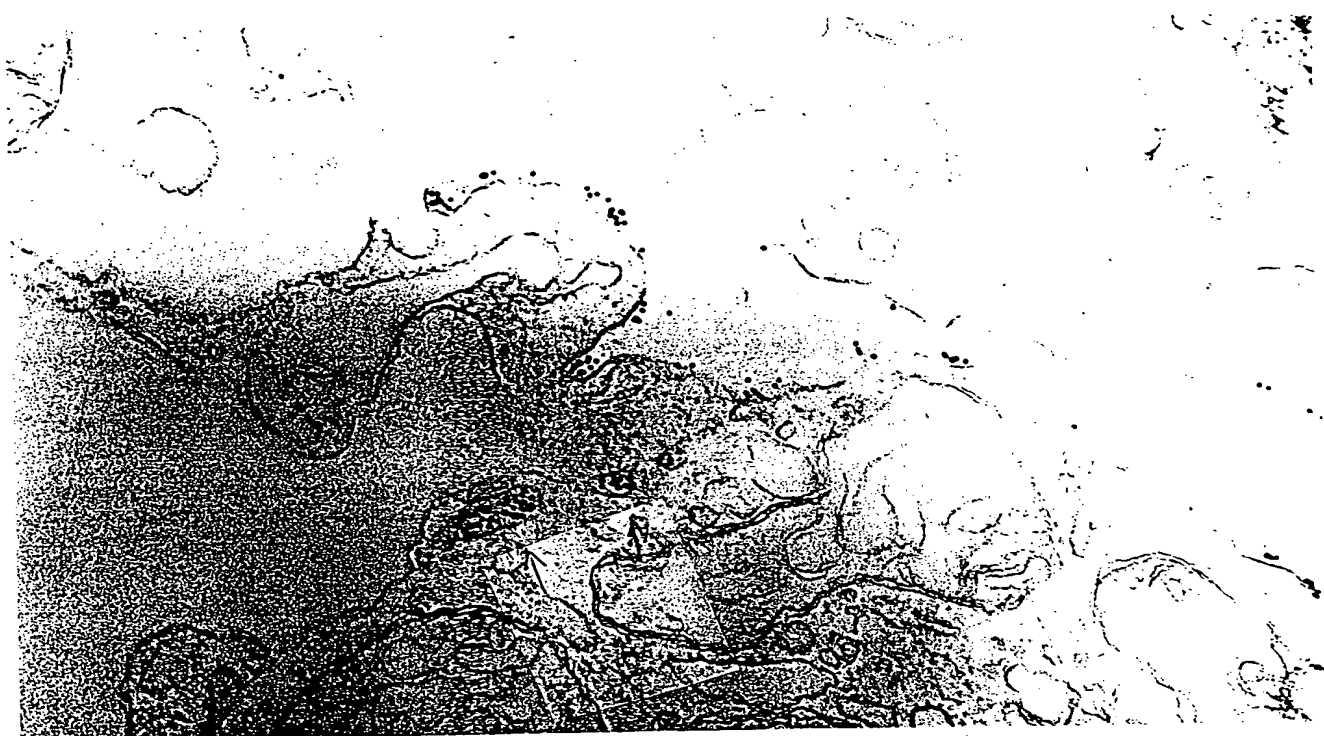


FIGURE 4

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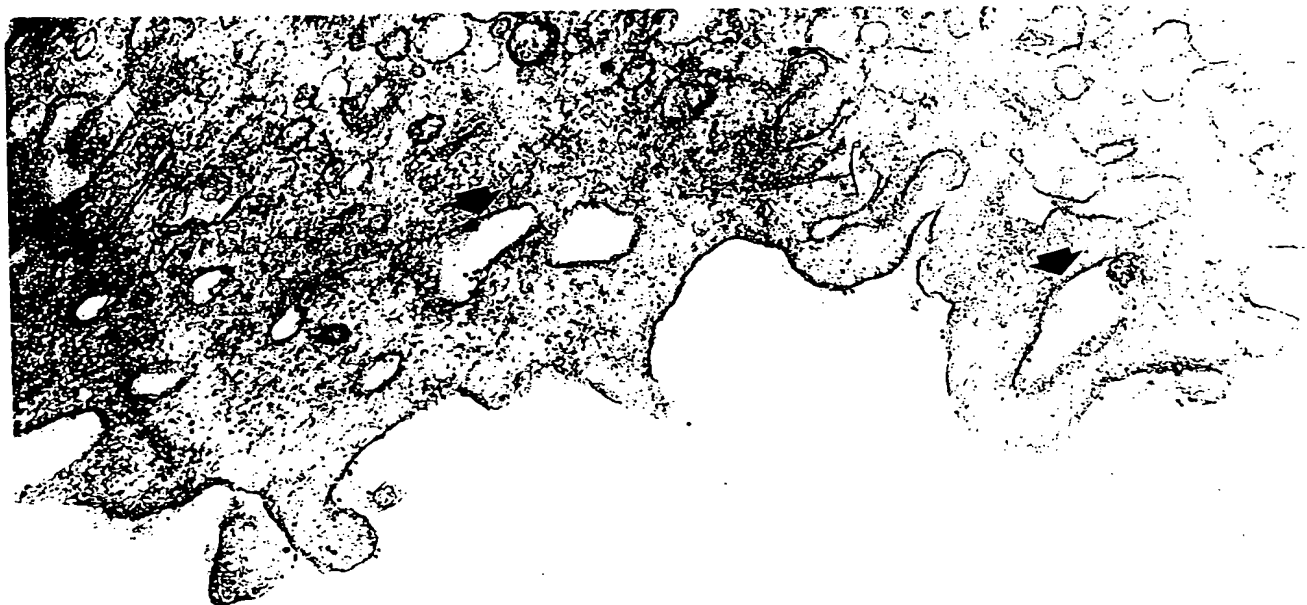


FIGURE 5

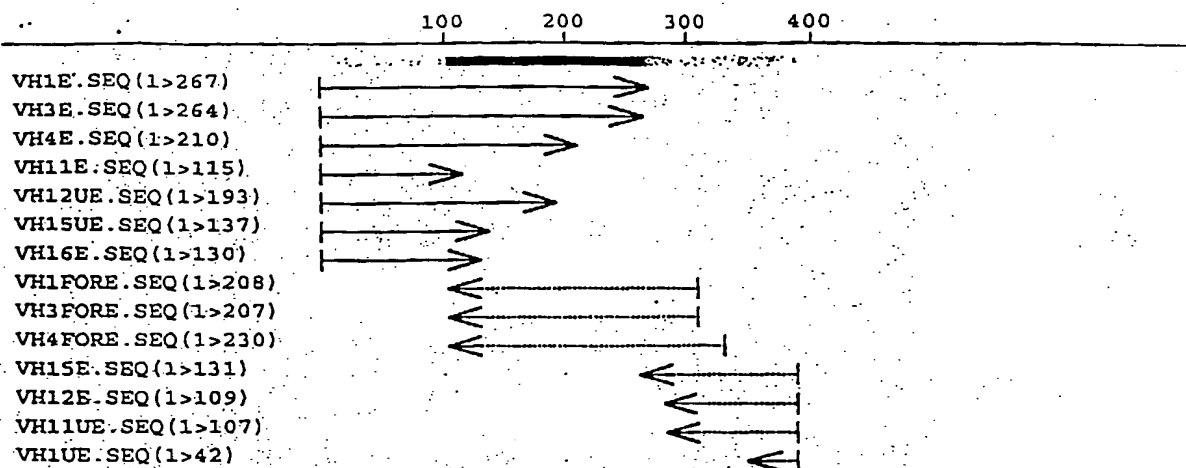


FIGURE 6

Enzymes: All 74 enzymes (No Filter)
Settings: Linear, Certain Sites Only, Standard Genetic Code

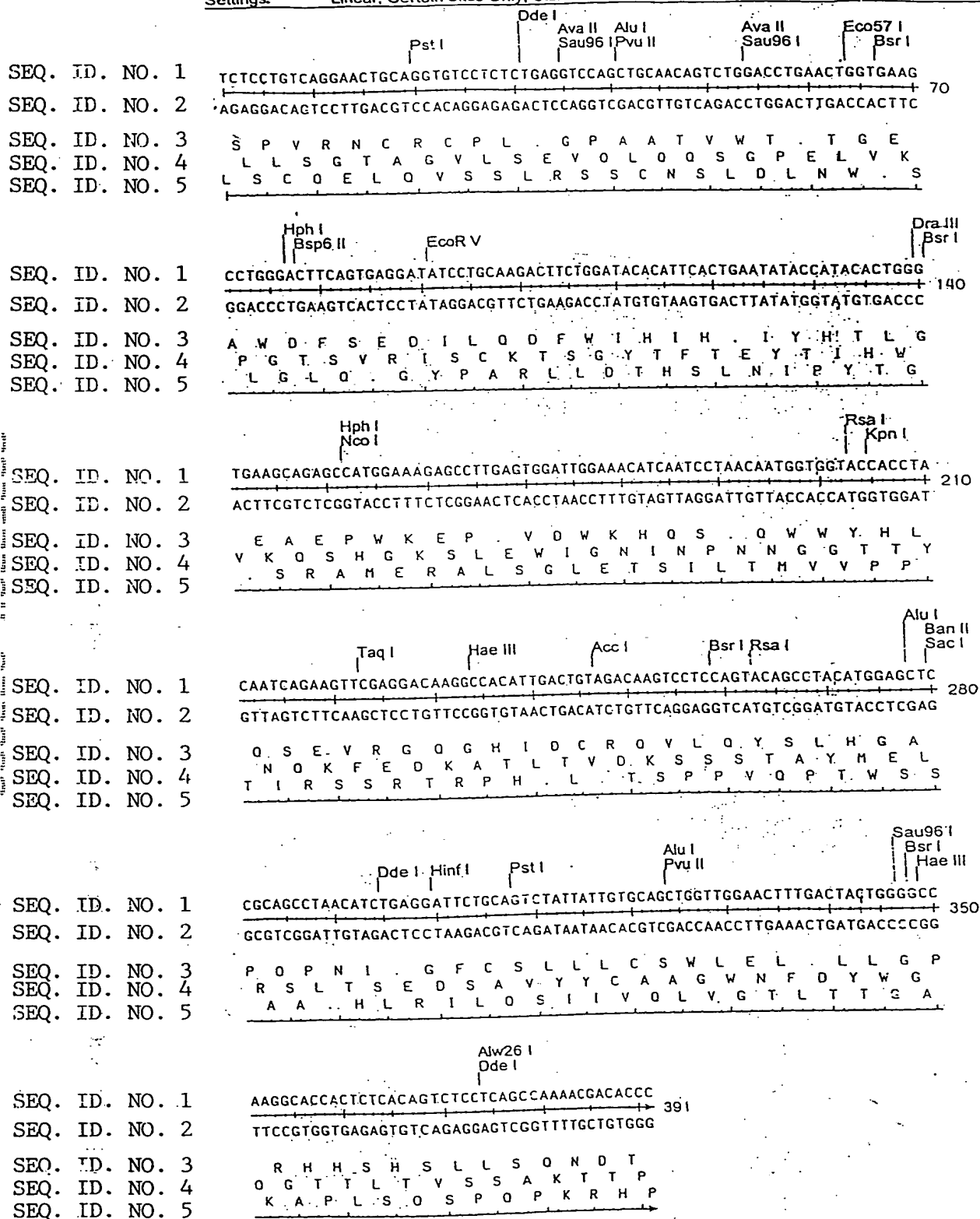


FIGURE 7

Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>115)	Seq2(1>125)	Similarity Index	Gap Number	Gap Length	Consensus Length
J591VH.PRO	MUVHIIA.PRO	75.6	2	10	125
(1>115)	(1>125)				

```

      10      20      30      40      50
EVQLQQSGPELVKPGTSVRISCKTSGYTFEYTI-HWVKQSHGKSLEWIGNINPNNGGTT
EVQLQQSGPELVKPG:SV:ISCK:SGYTFT:Y : :WVKQS.GKSLEWIG:INP.NGGT:
EVQLQQSGPELVKPGASVKISCKASGYFTDYYMNNWVKOSPGKSLEWIGDINPGNGGTS
      10      20      30      40      50      60
60      70      80      90      100      110
YNQKFEDKATLTVDKSSSTAYMELRSLTSEDSAVYYCAAG-----WNFDYWGGGTT
YNQKF :KATLTVDKSSSTAYM:L.SLTSEDSAVYYCA G      FDYWGGGTT
YNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARGYYSSSYMAYYAFDYWGQGT
      70      80      90      100      110      120

```

LTVSS
:TVSS
VTVSS

FIGURE 8

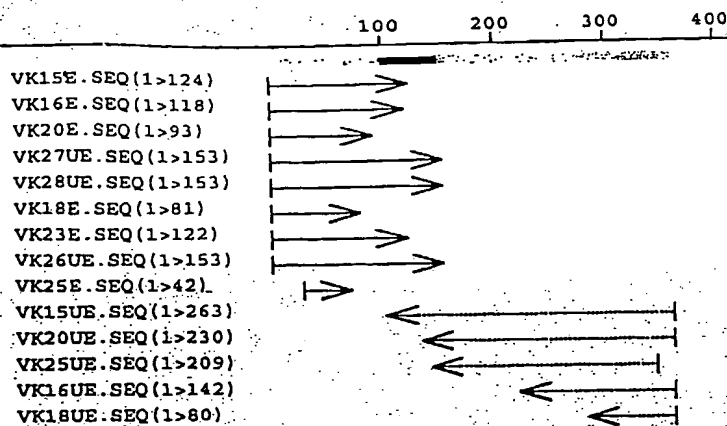


FIGURE 9

Enzymes: All 74 enzymes (No Filter)
Settings: Linear, Certain Sites Only, Standard Genetic Code

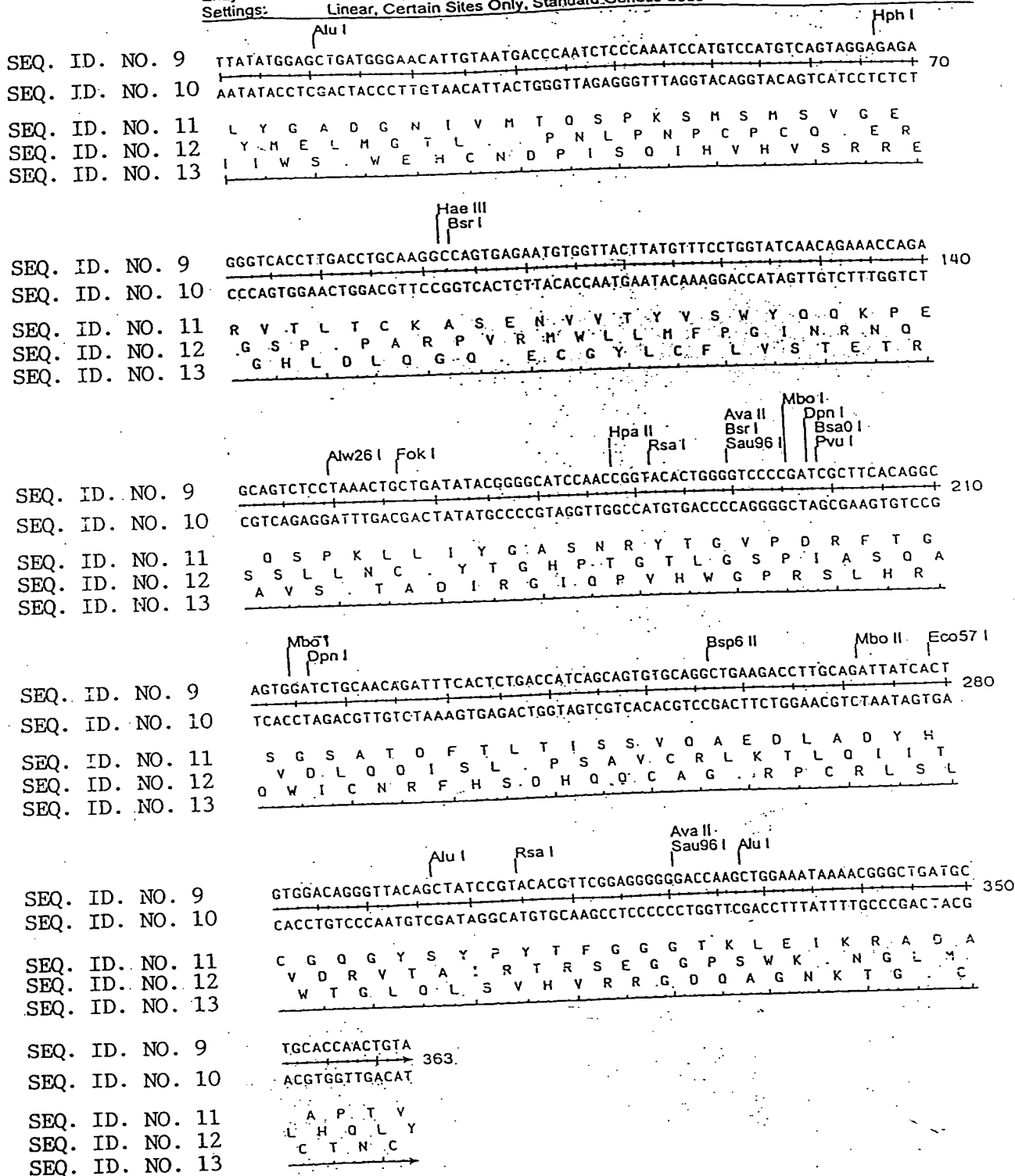


FIGURE 10

Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>107)	Seq2(1>111)	Similarity Index	Gap Number	Gap Length	Consensus Length
J591VK.PRO	MUVKV.PRO				
(1>107)	(1>109)	60.4	2	2	109
<div> <div>10</div> <div>20</div> <div>30</div> <div>40</div> <div>50</div> </div> <div> <div>60</div> <div>70</div> <div>80</div> <div>90</div> <div>100</div> </div>					
NIVMTQSPKSMMSVGERVTLTCKAS-ENVVTVVSWYQQKPEQSPKLLIYGASNRYTGVP					
:I MTQSP.S:S S:G:RVT:TC:AS :::Y::WYQQKP.SPKLLIY AS.:GVP					
DIOMTQSPSSLSASLGDRVTITCRASODDISNYLNWYQQKPGGSPKLLIYYASRLHSGVP					
DRFTGSGSATDFTLTISSSVOAEDLADYHCGGGYSY-PYTFGGGKLEIK					
RF:GSGS:TD::LTIS:::ED:A.Y C QG::P TFGGGKLEIK					
SRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPRTFGGGKLEIK					

FIGURE 11